

SEQUENCE LISTING

<110> Sims, John E.
Smith, Dirk E.

<120> IL-1 RECEPTOR ACCESSORY PROTEIN

<130> 3151-A

<140> --to be assigned--

<141> 2001-10-26

<150> US 60/244,831

<151> 2000-10-31

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2064)

<223>

<220>

<221> misc_feature

<222> (1792)..(1792)

<223> "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.

<400> 1

atg	aca	ctt	ctg	tgg	tgt	gta	gtg	agt	ctc	tac	ttt	tat	gga	atc	ctg	48
Met	Thr	Leu	Leu	Trp	Cys	Val	Val	Ser	Leu	Tyr	Phe	Tyr	Gly	Ile	Leu	
1				5				10					15			

caa	agt	gat	gcc	tca	gaa	cgc	tgc	gat	gac	tgg	gga	cta	gac	acc	atg	96
Gln	Ser	Asp	Ala	Ser	Glu	Arg	Cys	Asp	Asp	Trp	Gly	Leu	Asp	Thr	Met	
			20				25					30				

agg	caa	atc	caa	gtg	ttt	gaa	gat	gag	cca	gct	cgc	atc	aag	tgc	cca	144
Arg	Gln	Ile	Gln	Val	Phe	Glu	Asp	Glu	Pro	Ala	Arg	Ile	Lys	Cys	Pro	
		35					40					45				

ctc	ttt	gaa	cac	ttc	ttg	aaa	ttc	aac	tac	agc	aca	gcc	cat	tca	gct	192
Leu	Phe	Glu	His	Phe	Leu	Lys	Phe	Asn	Tyr	Ser	Thr	Ala	His	Ser	Ala	
		50				55					60					

ggc	ctt	act	ctg	atc	tgg	tat	tgg	act	agg	cag	gac	cgg	gac	ctt	gag	240
Gly	Leu	Thr	Leu	Ile	Trp	Tyr	Trp	Thr	Arg	Gln	Asp	Arg	Asp	Leu	Glu	
65					70				75					80		

gag	cca	att	aac	ttc	cgc	ctc	ccc	gag	aac	cgc	att	agt	aag	gag	aaa	288
Glu	Pro	Ile	Asn	Phe	Arg	Leu	Pro	Glu	Asn	Arg	Ile	Ser	Lys	Glu	Lys	
				85				90						95		

10061727-100601

gat gtg ctg tgg ttc cgg ccc act ctc ctc aat gac act ggc aac tat 336
 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
 100 105 110

acc tgc atg tta agg aac act aca tat tgc agc aaa gtt gca ttt ccc 384
 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
 115 120 125

ttg gaa gtt gtt caa aaa gac agc tgt ttc aat tcc ccc atg aaa ctc 432
 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
 130 135 140

cca gtg cat aaa ctg tat ata gaa tat ggc att cag agg atc act tgt 480
 Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
 145 150 155 160

cca aat gta gat gga tat ttt cct tcc agt gtc aaa ccg act atc act 528
 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
 165 170 175

tgg tat atg ggc tgt tat aaa ata cag aat ttt aat aat gta ata ccc 576
 Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
 180 185 190

gaa ggt atg aac ttg agt ttc ctc att gcc tta att tca aat aat gga 624
 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
 195 200 205

aat tac aca tgt gtt gtt aca tat cca gaa aat gga cgt acg ttt cat 672
 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
 210 215 220

ctc acc agg act ctg act gta aag gta gta ggc tct cca aaa aat gca 720
 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
 225 230 235 240

gtg ccc cct gtg atc cat tca cct aat gat cat gtg gtc tat gag aaa 768
 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
 245 250 255

gaa cca gga gag gag cta ctc att ccc tgt acg gtc tat ttt agt ttt 816
 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
 260 265 270

ctg atg gat tct cgc aat gag gtt tgg tgg acc att gat gga aaa aaa 864
 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
 275 280 285

cct gat gac atc act att gat gtc acc att aac gaa agt ata agt cat 912
 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
 290 295 300

agt aga aca gaa gat gaa aca aga act cag att ttg agc atc aag aaa 960
 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
 305 310 315 320

gtt acc tct gag gat ctc aag cgc agc tat gtc tgt cat gct aga agt 1008
 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
 325 330 335

gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca 1056
Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
340 345 350

gct cca aga tac aca gtg gaa ctg gct tgt ggt ttt gga gcc aca gtc 1104
Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365

ctg cta gtg gtg att ctc att gtt gtt tac cat gtt tac tgg cta gag 1152
Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380

atg gtc cta ttt tac cgg gct cat ttt gga aca gat gaa acc att tta 1200
Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400

gat gga aaa gag tat gat att tat gta tcc tat gca agg aat gcg gaa 1248
Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
405 410 415

gaa gaa gaa ttt gta tta ctg acc ctc cgt gga gtt ttg gag aat gaa 1296
Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430

ttt gga tac aag ctg tgc atc ttt gac cga gac agt ctg cct ggg gga 1344
Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445

aat aca gtg gaa gca gtt ttt gat ttc att cag aga agc aga agg atg 1392
Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
450 455 460

att gtt gtt ctg agc cct gac tat gtg aca gaa aag agc atc agc atg 1440
Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
465 470 475 480

ctg gag ttt aaa ctg ggt gtc atg tgc cag aac tcc att gcc acc aag 1488
Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
485 490 495

ctc att gtg gtt gag tac cgt ccc ctt gag cac ccg cac cca ggc att 1536
Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
500 505 510

ctt cag ctc aaa gag tct gtg tct ttt gtg agc tgg aag gga gaa aag 1584
Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
515 520 525

tcc aaa cat tct ggc tct aaa ttc tgg aaa gct ttg cgg ttg gct ctt 1632
Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
530 535 540

ccc ctg aga agt ctg agt gcc agt tct ggc tgg aat gag agc tgc tct 1680
Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
545 550 555 560

tcc cag tct gac atc agt ctg gat cac gtt caa agg agg aga agt cgt 1728
Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
565 570 575

ttg aaa gag ccc cca gaa ctt cag agc tca gag agg gct gca ggt agc 1776
Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
580 585 590

cct cca gcc cca ggc nca atg tcc aag cac cga ggg aag tcc tcc gcc 1824
Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
595 600 605

acc tgc cgc tgt tgt gtc acc tac tgt gaa gga gag aat cac ctt agg 1872
Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
610 615 620

aac aag agc cgg gca gag att cat aac cag ccc cag tgg gag aca cac 1920
Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
625 630 635 640

ctc	tgt	aag	cct	gtt	ccc	caa	gag	tca	gaa	act	caa	tgg	ata	caa	aat	1968
Leu	Cys	Lys	Pro	Val	Pro	Gln	Glu	Ser	Glu	Thr	Gln	Trp	Ile	Gln	Asn	.
				645					650					655		

ggc acc aga ttg gaa ccc cct gct ccc cag atc tca gcc ctt gct ctt 2016
Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
660 665 670

cat cat ttc acg gac tta tcc aat aac aac gac ttt tat atc cta taa 2064
His His Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
675 680 685

$\langle 210 \rangle$ 2

<211> 687

<212> PRT

<213> Homo sapiens

<220>

```
<221> misc_feature
```

 $\langle 222 \rangle \quad (598) \dots (598)$

<223> The 'Xaa' at location 598 stands for Thr or Pro.

<400> 2

Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
1 5 10 15

Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
35 40 45

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
130 135 140

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
165 170 175

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
180 185 190

Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
210 215 220

Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225 230 235 240

Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
245 250 255

Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
260 265 270

Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
290 295 300

Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
325 330 335

Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
340 345 350

Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365

Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
500 505 510

Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
530 535 540

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
545 550 555 560

10061727-102604

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
565 570 575

Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
580 585 590

Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
595 600 605

Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
610 615 620

Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
625 630 635 640

Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn
645 650 655

Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
660 665 670

His His Phe Thr Asp Leu Ser Asn Asn Asp Phe Tyr Ile Leu
675 680 685

<210> 3
<211> 2058
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(2058)
<223>

<400> 3
atg gga ctt ctg tgg tat ttg atg agt ctg tcc ttc tat ggg atc ctg 48
Met Gly Leu Leu Trp Tyr Leu Met Ser Leu Ser Phe Tyr Gly Ile Leu
1 5 10 15

cag agt cat gct tcg gag cgc tgt gat gac tgg gga cta gat acc atg 96
Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
20 25 30

cga caa atc caa gtg ttt gaa gat gag ccg gct cga atc aag tgc ccc 144
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
35 40 45

ctc ttt gaa cac ttc ctg aag tac aac tac agc act gcc cat tcc tct 192
Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser
50 55 60

8

tct tca acg gaa gat gaa aca agg act cag att ttg agc atc aag aaa	960
Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys	
305 310 315 320	
gtc acc ccg gag gat ctc agg cgc aac tat gtc tgt cat gct cga aat	1008
Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn	
325 330 335	
acc aaa ggg gaa gct gag cag gct gcc aag gtg aaa cag aaa gtc ata	1056
Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile	
340 345 350	
cca cca agg tac aca gta gaa ctc gcc tgt ggt ttt gga gcc acg gtc	1104
Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val	
355 360 365	
ttt ctg gta gtg gtt ctc att gtg gtt tac cat gtt tac tgg ctg gag	1152
Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu	
370 375 380	
atg gtc ctc ttt tac cga gct cac ttt gga aca gat gaa aca att ctt	1200
Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu	
385 390 395 400	
gat gga aag gag tat gat att tat gtt tcc tat gca aga aat gtg gaa	1248
Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Val Glu	
405 410 415	
gaa gag gaa ttt gtg ctg ctg acg ctg cgt gga gtt ttg gag aat gag	1296
Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu	
420 425 430	
ttt gga tac aag ctg tgc atc ttc gac aga gac agc ctg cct ggg gga	1344
Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly	
435 440 445	
aat acc gtg gaa gca gtt ttt gat ttc att cag agg agc cga agg atg	1392
Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met	
450 455 460	
att gtt gtc ctg agc cct gac tat gtg aca gaa aag agc atc agc atg	1440
Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met	
465 470 475 480	
ctg gag ttt aag ctg ggt gtc atg tgc cag aac tcc att gcc act aag	1488
Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys	
485 490 495	
ctc att gtg gtg gag tac cgt ccg ctt gag caa ccc cat cca ggc atc	1536
Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile	
500 505 510	
atg cag ctg aag gag tct gtg tct ttt gta agc tgg aag gga gaa aag	1584
Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys	
515 520 525	
tcc aaa cat tct ggc tcc aag ttc tgg aag gcc ttg cgt ttg gct ctt	1632
Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu	
530 535 540	

ccc ctg aga agt ctg agc gcc agc tcc ggc tgg aat gag agc tgt tct 1680
 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
 545 550 555 560

tct cag tct gac atc agt ctg gat cat gtt cag agg aga agt cgt ttg 1728
 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu
 565 570 575

aaa gag ccc cca gaa ctc cga agc tca gag agg gtg tct gga gca gag 1776
 Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu
 580 585 590

cca gcc ccg ggc acg atg tcc aag cac cga ggg aaa ccc tca gca gcc 1824
 Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala
 595 600 605

tgt cgc tgc tgt gtc acc tac tgt gaa gga gaa agt cac ctc agg agc 1872
 Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser
 610 615 620

aag agc cgg gca gag atg cac acg cat ccc cag tgg gaa aca cac ctc 1920
 Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu
 625 630 635 640

tgt aag cct cct ctc caa gag tct gaa agt cag tgg ata caa aat ggc 1968
 Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly
 645 650 655

acc cga ccc gaa ccc gct ccc cag atc tca gct ctt gca ctc cgc cac 2016
 Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His
 660 665 670

ttt aca gat tta tcc aat aac aat gac ttt tat atc cta taa 2058
 Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
 675 680 685

<210> 4
 <211> 685
 <212> PRT
 <213> Mus musculus

<400> 4

Met Gly Leu Leu Trp Tyr Leu Met Ser Leu Ser Phe Tyr Gly Ile Leu
 1 5 10 15

Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
 20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
 35 40 45

Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser
 50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe
130 135 140

Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr
165 170 175

Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro
180 185 190

Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His
210 215 220

Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala
225 230 235 240

Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys
245 250 255

Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe
260 265 270

Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
275 280 285

Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr
290 295 300

10064727-102501

Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320

Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn
325 330 335

Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile
340 345 350

Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365

Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Val Glu
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile
500 505 510

Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
530 535 540

10064727 102601

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
545 550 555 560

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu
565 570 575

Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu
580 585 590

Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala
595 600 605

Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser
610 615 620

Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu
625 630 635 640

Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly
645 650 655

Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His
660 665 670

Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
675 680 685